

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:11:58 ; Search time 8.22857 Seconds
(without alignments)
91.441 Million cell updates/sec

Title: US-09-905-691-4

Perfect score: 16

Sequence: 1 ARRAAARARRAEEA 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	7	43.8	263	1	CCMC_BRAJA
2	7	43.8	291	1	YM32_MYCTU
3	7	43.8	381	1	ARGU_METHA
4	7	43.8	387	1	ARGU_METHA
5	7	43.8	417	1	PROA_MEIRU
6	7	43.8	423	1	CES5_HUMAN
7	7	43.8	428	1	Y486_MYCLE
8	7	43.8	444	1	VGLX_HSVBS
9	7	43.8	474	1	Y486_MYCTU
10	7	43.8	480	1	EX7L_RHILO
11	7	43.8	521	1	US26_HCMVA
12	7	43.8	603	1	HEML_AGABI
13	7	43.8	621	1	UL47_HSVBP
14	7	43.8	742	1	UL47_HSVBP
15	7	43.8	777	1	VGLB_PVIF
16	7	43.8	913	1	VGLB_PVIF
17	7	43.8	1318	1	HAP_HAEN
18	7	43.8	1394	1	RAP_HAEN
19	7	43.8	2390	1	SPCP_HUMAN
20	7	43.8	4523	1	DIHE_HUMAN
21	6	37.5	68	1	RPOZ_NEIMA
22	6	37.5	88	1	RPOZ_HAEN
23	6	37.5	89	1	RPOZ_PASMU
24	6	37.5	90	1	RPOZ_VIBCH
25	6	37.5	90	1	RPOZ_VIBPA
26	6	37.5	90	1	RPOZ_VIBVU
27	6	37.5	91	1	RPOZ_ECOLI
28	6	37.5	91	1	RPOZ_YERPE
29	6	37.5	94	1	R28A_MYCTU
30	6	37.5	108	1	NIEW_RHOSH
31	6	37.5	113	1	UL67_HCMVA
32	6	37.5	117	1	RL18_HAEN
33	6	37.5	117	1	VGLJ_HSVBS

34 37.5 120 1 PAND_ALCEU
35 37.5 120 1 PAND_RALSO
36 37.5 122 1 CEF_CANFA
37 37.5 130 1 RS11_SYNPF
38 37.5 130 1 RS8_PSEAE
39 37.5 134 1 RK16_PINTH
40 37.5 135 1 NIUL_RHOCA
41 37.5 139 1 LPOV_MYCTU
42 37.5 143 1 Y880_MYCLE
43 37.5 143 1 Y880_MYCTU
44 37.5 143 1 RL32_AERPE
45 37.5 145 1 YV40_DEIRA

ALIGNMENTS

RESULT 1
CCMC_BRAJA
ID CCMC_BRAJA STANDARD; PRT; 263 AA.
AC P30962;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Heme exporter protein C (Cytochrome c-type biogenesis protein cycz).
GN CYCZ OR CCMC OR BLR0469.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=110RIF15;
RX MEDLINE=91210304; PubMed=1850420;
RA Ramseier T.N., Winteler H.V., Hennecke H.;
RT "Discovery and sequence analysis of bacterial genes involved in the
RT biogenesis of c-type cytochromes.";
RL J. Biol. Chem. 266:7793-7803(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
CC -!- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE
CC BIOGENESIS OF C-TYPE CYTOCHROMES.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- SIMILARITY: BELONGS TO THE CCMC/CYCZ/HELC FAMILY.
CC
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CC
CC EMBL; M60874; AAA26194.1;
CC EMBL; AF005936; BAC45734.1;
CC PIR; C39741; C39741.
CC InterPro: IPR002541; CytC_asm.
CC InterPro: IPR003557; CytC_blog_CcmC.
CC Pfam: PF01578; CytC_asm; 1.
CC PRINTS; PR01386; CCMCBIOGNIS.
CC TIGRFAM; TIGR01191; ccmC; 1.
CC Cytochrome c-type biogenesis; Transport; Transmembrane;
CC Inner membrane; Complete proteome.
KW

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FT TRANSMEM 19 39 POTENTIAL.
FT TRANSMEM 61 81 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 126 146 POTENTIAL.
FT TRANSMEM 157 177 POTENTIAL.
FT TRANSMEM 198 218 POTENTIAL.
SQ SEQUENCE 263 AA; 28831 MW; A02EF75769F94ECO CRC64;

Query Match 43.8%; Score 7; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAAA 9
      |||||
DB 151 RAARAAA 157

RESULT 2
YMS2_MCTU STANDARD; PRT; 291 AA.
ID YMS2_MCTU
AC Q10515; Q10516;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2232/RV2233.
DE RV2232/RV2233 OR MT2292 OR MTCY427.13/MTCY427.14.
GS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
[2]
RS SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Hart D., Hickey E.,
RA Kolonay J.J., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/VIEH FAMILY.
CC -----
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CC -----
DB EMBL; Z70692; CAA94666.1; ALT_TERM.
DR EMBL; Z70692; CAA94665.1; ALT_INIT.
DR EMBL; AE007074; AAK46576.1; -.
DR TIGR; MT2292; -.
DR TubercuList; RV2232; -.
DR TubercuList; RV2233; -.
DR InterPro; IPR005834; Hydrolase.

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Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AAAAAAAR 10
Db 13 AAAAAAAR 19

RESULT 6
CES5 HUMAN STANDARD; PRT; 423 AA.
AC Q9BXW7; Q9BXW8; Q9NWA8; Q9N4X1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cat eye syndrome critical region protein 5 precursor.
GN CECR5
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=21275466; PubMed=11381032;
RA Footz T.K., Brinkman-Mills P., Banting G.S., Maier S.A., Riaz M.A.,
RA Brigland L.J., Hu S., Birren B., Minoshima S., Shimizu N., Pan H.,
RA Nguyen T., Fang F., Fu Y., Ray L., Wu H., Shaull S., Phan S., Yao Z.,
RA Chen F., Huan A., Hu P., Wang Q., Loh P., Qi S., Roe B.A.,
RA McDermid H.E.
RT *Analysis of the cat eye syndrome critical region in humans and the
RT region of conserved synteny in mice: a search for candidate genes at
RT or near the human chromosome 22 pericentromere.*;
RL Genome Res. 11:1053-1070(2001).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Embryo, and Gastric carcinoma;
RA Isozaki T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Takagishima M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT *NEO human cDNA sequencing project.*;
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Lymph;
RX PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schell J.E., Jones S.J.M., Marra M.A.;
RT *Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.*;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- ALTERNATIVE PRODUCTS;
CC Event-Alternative splicing; Named isoforms-2;
CC Name-2;
CC IsoId-Q9BXW7-1; Sequence-Displayed;

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CC Name-1;
CC IsoId-Q9BXW7-2; Sequence-VSP_003840;
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- MISCELLANEOUS: Candidate gene for the Cat Eye Syndrome (CES), a
CC developmental disorder associated with the duplication of a 2 Mb
CC region of 22q11.2. Duplication usually takes in the form of a
CC surpernumerary bisatellited isodicentric chromosome, resulting in
CC four copies of the region (represents an inv dup(22)(q11)). CES is
CC characterized clinically by the combination of coloboma of the
CC iris and anal atresia with fistula, downslanting palpebral
CC fissures, preauricular tags and/or pits, frequent occurrence of
CC heart and renal malformations, and normal or near-normal mental
CC development.
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CC -----
CC EMBL; AF273271; AAK19152.1; -
CC EMBL; AF273270; AAK19151.1; -
CC EMBL; AK001034; BAA91475.1; -
CC EMBL; AK000461; BAA91180.1; -
CC EMBL; BC042540; BAA92540.1; -
CC Genew; HGNC:1843; CECR5.
CC InterPro; IPR006353; HAD_CECR5.
CC InterPro; IPR006357; HAD_SF_IIA.
CC TIGRFAMs; TIGR01456; CECR5; 1.
CC TIGRFAMs; TIGR01460; HAD-SF-IIA; 1.
CC Signal; Alternative splicing. POTENTIAL.
CC SIGNAL 1 23
CC CHAIN 24 423
CC CAT EYE SYNDROME CRITICAL REGION PROTEIN
CC VARSPLIC 1 41
CC -----
CC -> MYAWEFLP9FS (in isoform 1).
CC /FTIG-VSP_003840.
CC D -> N (IN REF. 2; BAA91180).
CC V -> F (IN REF. 2; BAA91475).
CC E -> G (IN REF. 2; BAA91475).
CC SEQUENCE 423 AA; 46321 MW; C4D9208AB8B8CCE CRC64;
SQ
Query Match 43.8%; Score 7; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 RAARAAA 9
Db 19 RAARAAA 25
-----
RESULT 7
Y486_MYCLE
ID Y486_MYCLE STANDARD; PRT; 428 AA.
AC P54138; Q9CB50;
DT 01-OCT-1995 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein ML2443.
GN ML2443 OR U2168F OR B2168_C2_201.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-TN;

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RX MEDLINE-21128732; PubMed-11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Halroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -1- SIMILARITY: TO M.TUBERCULOSIS RV0486.
CC -----
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CC -----
DR EMBL; U00018; AAA17228.1; ALT_INIT.
DR EMBL; AL583925; CAC31960.1; -.
DR PIR; H87214; H87214.
DR Leproma; ML2443; -.
DR InterPro; IPR001296; Glyco_transf.1.
DR Pfam; PF00534; Glycos_transf.1; 1.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 428 AA; 45291 MW; A14F9F0187E3587C CRC64;

Query Match 43.8%; Score 7; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAARA 8
Db 204 RRAARA 210

RESULT 8
VGLX_HSVBS STANDARD; PRT; 444 AA.
ID VGLX_HSVBS
AC Q08103;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein GX precursor.
OS Bovine herpesvirus type 1.2 (strain ST).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=45407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94167875; PubMed-8122370;
RA Leung-Tack P., Audonnet J.F., Riviere M.;
RT "The complete DNA sequence and the genetic organization of the short
RT unique region (US) of the bovine herpesvirus type 1 (ST strain).";
RL Virology 195:409-421(1994).
CC -----
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CC -----
DR EMBL; Z23068; CAA80603.1; -.
DR PIR; S35783; S35783.
DR InterPro; IPR003363; Herpes_gg.
DR Pfam; PF02400; Herpes_gg; 1.
KW Glycoprotein; Transmembrane; Signal.

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FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 444 GLYCOPROTEIN GX.
FT TRANSMEM 390 414 POTENTIAL.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 444 AA; 46708 MW; 0145942AA35B05CB CRC64;

Query Match 43.8%; Score 7; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AARRARA 14
Db 422 AARRARA 428

RESULT 9
CYAE_BORPE STANDARD; PRT; 474 AA.
ID CYAE_BORPE
AC P11092;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein cyae precursor.
GN CYAE.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=18323;
RX MEDLINE-89091151; PubMed-2905265;
RA Glaser P., Sakamoto H., Bellalou J., Ullmann A., Danchin A.;
RT "Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-
RT haemolysin bifunctional protein of Bordetella pertussis.";
RL EMBO J. 7:3997-4004(1988).
CC -1- FUNCTION: CYAE IS NECESSARY FOR TRANSPORT OF CALMODULIN-SENSITIVE
CC ADENYLATE CYCLASE-HEMOLYSIN (CYCLOLYSIN).
CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PRTE FAMILY OF SECRETION PROTEINS.
CC -----
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CC -----
DR EMBL; X14199; CAA32414.1; -.
DR PIR; S02388; BVBRCE.
DR InterPro; IPR003423; OEP.
DR Pfam; PF02321; OEP; 2.
KW Hemolysis; Transport; Outer membrane; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 474 PROTEIN CYAE.
SQ SEQUENCE 474 AA; 50204 MW; 29AA4F21D377FC957 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AARRARA 14
Db 203 AARRARA 209

RESULT 10
Y486_MYCTU STANDARD; PRT; 480 AA.
ID Y486_MYCTU
AC Q11152;

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein RV0486.
GN RV0486 OR MT0504 OR MTCV20G9.12.
OS Mycobacterium tuberculosis
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.F., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RT Nature 393:537-544(1998).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=CDC 1551 / Oshkosh;
RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Petersohn J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [1]
RN SIMILARITY: TO M. LEPRAE ML2443.
CC -----
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CC -----
CC EMBL: Z77162; CAB00947.1; -;
CC DR EMBL; A8006951; AAK44727.1; -;
CC DR EMBL; A70744; A70744.
CC DR TIGR: MT0504; -;
CC TubercuList; RV0486; -;
CC InterPro: IPR001296; Glyco_transf_1.
CC Pfam: PF00534; Glycos_transf_1; 1.
CC Hypothetical protein; Complete proteome.
KW SEQUENCE 480 AA; 50541 MW; 2134755E894A9CCF CRC64;
SQ
Query Match 43.8%; Score 7; DB 1; Length 480;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RRAAAA 8 PRT; 521 AA.
DB 252 RRAAAA 258
RESULT 11
EX7L_RHILO STANDARD; PRT; 521 AA.
ID AC Q987V3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
DE (Exonuclease VII large subunit).

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RL J. Mol. Biol. 192:177-208(1986).
RN [2]
RP COMPLETE GENOME.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
RA Reddick E., Satchwell S.C., Tomlinson P., Weston K.M., Barrett B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC -1- SIMILARITY: BELONGS TO THE US22 FAMILY.
CC
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CC
DR EMBL; X17403; CAA35293.1; -
DR EMBL; X04650; CAB37117.1; -
DR PIR; A27216; QQBEDI.
DR InterPro; IPR003360; US22.
DR Pfam; PF02393; US22; 1.
KW Hypothetical protein.
FT CARBOHYD 44 44 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 603 AA; 70020 MW; E34F64D01E27687C CRC64;

Query Match 43.88; Score 7; DB 1; Length 603;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAAA 8
DB 574 RRAAAA 580
|||||

RESULT 13
HEMI_AGABI STANDARD; PRT; 621 AA.
AC Q97403;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 5-aminolevulinic acid synthase, mitochondrial precursor (EC 2.3.1.37)
DE (Delta-aminolevulinic synthase) (Delta-ALA synthetase).
GN HEMI.
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OX NCBI_TaxID=5341;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D649;
RA Irgue E., Menak-zunic M., Wood D.A., Thurston C.F.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Succinyl-CoA + glycine -> 5-aminolevulinic acid + CO(2).
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Heme biosynthesis; first (rate-limiting) step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
CC
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CC EMBL; Z50096; CAA90424.1; -
DR InterPro; IPR003408; Ala_synthase.
DR InterPro; IPR004839; Aminotransf_2.
DR InterPro; IPR001917; NHtransf_2.
DR Pfam; PF02490; Ala_synthase; 1.
DR Pfam; PF00155; aminotran_1_2; 1.
DR PROSITE; PS00599; AA-TRANSFER_CLASS_2; 1.
KW Heme biosynthesis; Transferrase; Acyltransferase; Mitochondrion;
KW Transmembrane; Pyridoxal phosphate.
FT TRANSIT 1 ? MITOCHONDRION.
FT CHAIN ? 621 5-AMINOLEVULINIC ACID SYNTHASE.
FT BINDING 362 362 PYRIDOXAL PHOSPHATE (PROBABLE).
SQ SEQUENCE 621 AA; 67426 MW; A335C3268FAE1AA3 CRC64;

Query Match 43.88; Score 7; DB 1; Length 621;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAAAAA 10
DB 54 AAAAAA 60
|||||

RESULT 14
UL47_HSVBP STANDARD; PRT; 742 AA.
AC P30021;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 80.7 kDa alpha trans-inducing protein (VP8 tegument protein) (VP7
DE protein) (107 kDa protein).
GN VP8
OS Bovine herpesvirus type 1 (strain P8-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10324;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92113550; PubMed=1662698;
RA Carpenter D.E., Misra V.;
RT "The most abundant protein in bovine herpes 1 virions is a homologue
RT of herpes simplex virus type 1 UL47."
RL J. Gen. Virol. 72:3077-3084(1991).
CC -1- FUNCTION: MODULATOR OF ALPHA-TIF (VNM65 PHOSPHOPROTEIN) TRANS-
CC ACTIVATION. UL47 MAY HAVE KINASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: MAJOR TEGUMENT PROTEIN OF THE VIRIONS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE LATER STAGES OF INFECTION.
CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL47,
CC EBV-1 13, AND VZV 11.
CC
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CC
DR EMBL; D10327; BAA01170.1; -
DR EMBL; Z11610; CAA77683.1; -
DR PIR; JQ1435; TNBERI.
DR InterPro; IPR005029; Herpes_UL47.
DR Pfam; PF03362; Herpes_UL47; 1.
KW Transcription regulation; Trans-acting factor; Structural protein;
KW Late protein; Phosphorylation.
SQ SEQUENCE 742 AA; 80744 MW; 85979D8C2C953C89 CRC64;

Query Match 43.88; Score 7; DB 1; Length 742;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 AAAAAA 10
DB 376 AAAAAA 382

DB 770 AAAAAA 776

Search completed: August 9, 2003, 16:29:51
Job time : 8.22857 secs

RESULT 15
METE_CAUCR
ID METE_CAUCR STANDARD; PRT; 777 AA.
AC Q9AAW1;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase
DE (EC 2.1.1.14) (Methionine synthase, vitamin-B12 independent isozyme)
DE (Cobalamin-independent methionine synthase).
GN METE OR CC0482.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RA MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA *Complete genome sequence of Caulobacter crescentus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RC -1- FUNCTION: Catalyzes the transfer of a methyl group from 5-
CC methyltetrahydrofolate to homocysteine resulting in methionine
CC formation (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-
CC homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine.
CC -1- COFACTOR: Zinc; binds one ion per subunit (By similarity).
CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
CC -1- SIMILARITY: Belongs to the vitamin-B12 independent methionine
CC synthase family.
CC -----
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CC -----
CC EMBL; AE005721; AAK22469.1; -
CC PIR; A87309; A87309.
CC TIGR; CC0482; -.
CC HAMAP; MF_00172; -.
CC InterPro; IPR002629; Methionine_synth.
CC InterPro; IPR006276; Met_syn_B12ind.
CC Pfam; PF01717; Methionine_synth; 1.
CC ProDom; PD004692; Methionine_synth; 2.
CC TIGRFAMs; TIGR01371; met_syn_B12ind; 1.
CC Transferrase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
CC Complete proteome.
CC METAL 665 665 ZINC (BY SIMILARITY).
CC METAL 667 667 ZINC (BY SIMILARITY).
CC METAL 750 750 ZINC (BY SIMILARITY).
CC SEQUENCE 777 AA; 84380 MW; 1C4D5FD7E80A80F3 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 777;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAAAA 14

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